

GenCore version 4.5

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OM nucleic - nucleic search, using sw model

Run on: January 18, 2002, 10:14:33 ; Search time 211.29 Seconds  
(without alignments)  
73.036 Million cell<sup>s</sup> updates/sec

Title: US-09-651-846-1  
Perfect score: 18  
Sequence: 1 gacgctggggccat 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428665619 residues

Total number of hits satisfying chosen parameters: 1026190  
Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq-1101.\*

1: /SIDS2/gcdata/geneseq/geneseq/NA1980.DAT:\*

2: /SIDS2/gcdata/geneseq/geneseq/NA1981.DAT:\*

3: /SIDS2/gcdata/geneseq/geneseq/NA1982.DAT:\*

4: /SIDS2/gcdata/geneseq/geneseq/NA1983.DAT:\*

5: /SIDS2/gcdata/geneseq/geneseq/NA1984.DAT:\*

6: /SIDS2/gcdata/geneseq/NA1985.DAT:\*

7: /SIDS2/gcdata/geneseq/NA1986.DAT:\*

8: /SIDS2/gcdata/geneseq/NA1987.DAT:\*

9: /SIDS2/gcdata/geneseq/NA1988.DAT:\*

10: /SIDS2/gcdata/geneseq/NA1989.DAT:\*

11: /SIDS2/gcdata/geneseq/NA1990.DAT:\*

12: /SIDS2/gcdata/geneseq/NA1991.DAT:\*

13: /SIDS2/gcdata/geneseq/NA1992.DAT:\*

14: /SIDS2/gcdata/geneseq/NA1993.DAT:\*

15: /SIDS2/gcdata/geneseq/NA1994.DAT:\*

16: /SIDS2/gcdata/geneseq/NA1995.DAT:\*

17: /SIDS2/gcdata/geneseq/NA1996.DAT:\*

18: /SIDS2/gcdata/geneseq/NA1997.DAT:\*

19: /SIDS2/gcdata/geneseq/NA1998.DAT:\*

20: /SIDS2/gcdata/geneseq/NA2000.DAT:\*

21: /SIDS2/gcdata/geneseq/NA2001.DAT:\*

22: /SIDS2/gcdata/geneseq/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	18	100.0	35 20	AMX36573 PCR primer for human LPA receptor/retat
C 2	18	100.0	35 22	AMX0266 Human TUB gene 3, Human tuftpl gene P
C 3	13.2	73.3	19 18	AMX6666 Human TX mutagenic Factor
C 4	13.2	73.3	19 21	AMX94661 Human TX mutagenic Factor
C 5	13.2	73.3	30 20	AMZ2576 Oligonucleotide us
C 6	13.2	73.3	30 20	AMZ25860 Human FAS/T1 gene
C 7	13.2	73.3	48 21	AMX46997 Primer used to amp
C 8	12.8	71.1	31 21	AMX58151 Primer used to amp
C 9	12.8	71.1	33 20	AMX59695 Human beta 1-4 gal
10	12.8	71.1	33 20	AMX5994 Human beta 1-4 gal
11	12.4	68.9	27 20	AMX80155

### ALIGNMENTS

RESULT ID	1	XX	XX	XX
	AMX36573	standard; DNA; 35 BP.	AC	AAX36573;
		DT 07-JUL-1999 (first entry)	XX	DE PCR primer for human EDG-1 coding sequence.
			XX	XX EDG-1; EDG-2; EDG-3; EDG-4; EDG-5; PSP-24; human; detection; therapy; inverse agonist; allosteric modulator; lysophosphatidic acid receptor; LPA signalling mediated disease; cellular apoptosis; PCR primer; ss.
			XX	OS Synthetic.
			XX	OS Home-septins.
			XX	OS WO9919513-A2.
			PD 22-APR-1999.	
			XX	PF 09-OCT-1998; 98W0-US21315.
			XX	PR 10-OCT-1997; 97US-0061572.
			XX	PA (LXR-B) LXR BIOTECHNOLOGY INC.
			XX	PI Erikson J, Goddard JG, Kiefer M;
			XX	DR WPI; 1999-277658/23.
			XX	PT Identification of (ant)agonists of LPA receptor EDG-2 for, e.g. treating LPA signalling mediated diseases such as cellular apoptosis

PS Example 1; Page 30; 63pp; English.

XX

CC

This sequence is a PCR primer for DNA encoding human EDG-1.

CC

The invention relates to methods of detecting (ant)agonist, inverse

CC

agonist or allosteric modulators of the lysophosphatidic acid receptors

CC

EDG-1, EDG-2, EDG-3, EDG-4, EDG-5, and PSP-24. The methods are used to

CC

identify (ant)agonists and allosteric modulator of the lysophosphatidic

CC

acid (LPA) EDG2 receptor, e.g. to treat LPA signalling mediated disease

CC

such cellular apoptosis.

CC

SQ Sequence 35 BP; 5 A; 15 C; 12 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 35;

Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gacgtcggtggcccat 18

DB 32 GACGCGGCGGGCCCAT 15

Query Match 100.0%; Score 18; DB 22; Length 35;

Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gacgtcggtggcccat 18

DB 32 GACGCGGCGGGCCCAT 15

RESULT 2

ID AAS0262

standard; DNA; 35 BP.

XX

CC bowel disease, and rejection of organ transplants.  
 XX sequence 35 BP; 5 A; 15 C; 12 G; 3 T; 0 other;  
 SQ

Query Match 100.0%; Score 18; DB 18; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 2e+03; Mismatches 0;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gacgtcggtggcccat 18

DB 32 GACGCGGCGGGCCCAT 15

RESULT 3

ID AAT9666/c |

XX AAT9666 standard; cDNA; 19 BP.

XX AAT9666;

XX 27-APR-1998 (first entry)

XX Human TUB gene 3' end primer for radiation hybrid mapping.

XX KW TULP; tub gene; human; sensory neuron; neurosensory defect; cochlear degeneration; hearing loss; deafness; retinal dystrophy; KW KW retinitis pigmentosa; combined rod cone dystrophy; obesity; KW animal model; transgenic animal; therapy; diagnosis; PCR; primer; KW ss.

XX OS Synthetic.

XX Homo sapiens.

XX WO973804-A1.

XX PD 16-OCT-1997.

XX PF 10-APR-1997; 97WO-US05903.

XX PR 17-SEP-1996; 96US-0714991.

PR 10-APR-1996; 96US-0030592.

PR 22-AUG-1996; 96US-0701380.

PR 04-SEP-1996; 96US-0706292.

XX (JACK-1) JACKSON LAB.

PA (SEQU-1) SEQUANA THERAPEUTICS INC.

XX PI Neagert J, Nishina P, Noben-Trauth K, North M;

XX WPI; 1997-512642/47.

XX Mammalian TULP protein - used for detecting pre-disposition to PT neuro-sensory defects

XX Disclosure; Page 35; 89pp; English.

XX PCR primers (AAT96663 and AAT96664) were designed for the 3' non-coding CC region of the human TUB gene (see AAT96639) and were used in CC radiation hybrid mapping, generating a product of 221 bp. Another CC primer pair (see AAT96661-6-62) amplified the 5' region of TUB, and a CC further pair (see AAT96665-6-66) amplified TULP1 cDNA (see AAT96642). CC TULP1 and TULP1 are novel members of the mammalian TULP gene family CC associated with various defects in sensory neurons such as cochlear defects, retinitis pigmentosa and combined rod-cone dystrophy.

XX Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 other;

PS The sequence represents the LPA receptor-related primer #1 used during analysis of lysophatidic acid receptor (LPA), EDG-2. The sequence is given in the specification but no further information is given. LPA is a phospholipid found in a variety of plant and animal products. EDG-2 is involved in cell signalling through activation of a Map kinase cascade-dependent reporter. Modulating the activity of a lysophosphatidic acid (LPA) or LPA receptor (EDG-2) involves introducing a composition comprising LPA modulators to the LPA or receptor. The method is useful for treating diseases characterised by slowed growth or repair of neuronal cells, neurodegenerative diseases, such as Alzheimer's disease, parkinson's disease, and acute neuron damage, for modulating apoptotic pathways and treating ischaemic heart disease, tumours, viral diseases



